

**RAW SEQUENCE LISTING
ERROR REPORT**

BIOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/835,521

Source: OIPE

Date Processed by STIC: 8-18-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/635,521

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
Indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING DATE: 08/18/2000
 PATENT APPLICATION: US/09/635,521 TIME: 14:12:07

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\08182000\I635521.raw

3 <110> APPLICANT: Katherine Galvin and Laura A. Rudolph-Owen
 5 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
 6 DIAGNOSIS OF CARDIOVASCULAR DISEASE USING GPCR 4941 AS
 7 A TARGET
 9 <130> FILE REFERENCE: MNI-094
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/635,521
 C--> 12 <141> CURRENT FILING DATE: 2000-08-09
 14 <150> PRIOR APPLICATION NUMBER: 60/199,908
 15 <151> PRIOR FILING DATE: 2000-04-26
 17 <160> NUMBER OF SEQ ID NOS: 3
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1362
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS /
 28 <222> LOCATION: (1)..(1359)
 30 <400> SEQUENCE: 1
 31 atg gct tca ccc agc ctc ccg ggc agt gac tgc tcc caa atc att gat 48
 32 Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp
 33 1 5 10 15
 35 cac agt cat gtc ccc gag ttt gag gtg gcc acc tgg atc aaa atc acc 96
 36 His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
 37 20 25 30
 39 ctt att ctg gtg tac ctg atc atc ttc gtg atg ggc ctt ctg ggg aac 144
 40 Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn
 41 35 40 45
 43 agc gcc acc att cgg gtc acc cag gtg ctg cag aag aaa gga tac ttg 192
 44 Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
 45 50 55 60
 47 cag aag gag gtg aca gac cac atg gtg agt ttg gct tgc tgc gac atc 240
 48 Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
 49 65 70 75 80
 51 ttg gtg ttc ctc atc ggc atg ccc atg gag ttc tac agc atc atc tgg 288
 52 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
 53 85 90 95
 55 aat ccc ctg acc acg tcc agc tac acc ctg tcc tgc aag ctg cac act 336
 56 Asn Pro Leu Thr Thr Ser Tyr Thr Leu Ser Cys Lys Leu His Thr
 57 100 105 110
 59 ttc ctc ttc gag gcc tgc agc tac gct acg ctg ctg cac gtg ctg aca 384
 60 Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
 61 115 120 125
 63 ctc agc ttt gag cgc tac atc gcc atc tgt cac ccc ttc agg tac aag 432
 64 Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
 65 130 135 140
 67 gct gtg tgc gga cct tgc cag gtg aag ctg ctg att ggc ttc gtc tgg 480

Does Not Comply
 Corrected Diskette Needed
 See P. 7

RAW SEQUENCE LISTING

DATE: 08/18/2000

PATENT APPLICATION: US/09/635,521

TIME: 14:12:07

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\08182000\I635521.raw

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68 Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
69 145 150 155 160
71 gtc acc tcc gcc ctg gtg gca ctg ccc ttg ctg ttt gcc atg ggt act 528
72 Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr
73 165 170 175
75 gag tac ccc ctg gtg aac gtg ccc agc cac cgg ggt ctc act tgc aac 576
76 Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn
77 180 185 190
79 cgc tcc agc acc cgc cac cac gag cag ccc gag acc tcc aat atg tcc 624
80 Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser
81 195 200 205
83 atc tgt acc aac ctc tcc agc cgc tgg acc gtg ttc cag tcc agc atc 672
84 Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile
85 210 215 220
87 ttc ggc gcc ttc gtg gtc tac ctc gtg gtc ctg ctc tcc gta gcc ttc 720
88 Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Ser Val Ala Phe
89 225 230 235 240
91 atg tgc tgg aac atg atg cag gtg ctc atg aaa agc cag aag ggc tcg 768
92 Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser
93 245 250 255
95 ctg gcc ggg ggc acg cgg cct ccg cag ctg agg aag tcc gag agc gaa 816
96 Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu
97 260 265 270
99 gag agc agg acc gcc agg agg cag acc atc atc ttc ctg agg ctg att 864
100 Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
101 275 280 285
103 gtt gtg aca ttg gcc gta tgc tgg atg ccc aac cag att cgg agg atc 912
104 Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
105 290 295 300
107 atg gct gcg gcc aaa ccc aag cac gac tgg acg agg tcc tac ttc cgg 960
108 Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg
109 305 310 315 320
111 gcg tac atg atc ctc ctc ccc ttc tcg gag acg ttt ttc tac ctc agc 1008
112 Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser
113 325 330 335
115 tcg gtc atc aac ccg ctc ctg tac acg gtg tcc tcg cag cag ttt cgg 1056
116 Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg
117 340 345 350
119 cgg gtg ttc gtg cag gtg ctg tgc cgc ctg tcg ctg cag cac gcc 1104
120 Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala
121 355 360 365
123 aac cac gag aag cgc ctg cgc gta cat gcg cac tcc acc acc gac agc 1152
124 Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser
125 370 375 380
127 gcc cgc ttt gtg cag cgc ccg ttg ctc ttc gcg tcc cgg cgc cag tcc 1200
128 Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser
129 385 390 395 400
131 tct gca agg aga act gag aag att ttc tta agc act ttt cag agc gag 1248
132 Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu

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RAW SEQUENCE LISTING

DATE: 08/18/2000

PATENT APPLICATION: US/09/635,521

TIME: 14:12:07

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\08182000\I635521.raw

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133                               405                               410                               415
135 gcc gag ccc cag tct aag tcc cag tca ttg agt ctc gag tca cta gag 1296
136 Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu
137                               420                               425                               430
139 ccc aac tca ggc gcg aaa cca gcc aat tct gct gca gag aat ggt ttt 1344
140 Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe
141                               435                               440                               445
143 cag gag cat gaa gtt tga 1362
144 Gln Glu His Glu Val
145 450
148 <210> SEQ ID NO: 2
149 <211> LENGTH: 453
150 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
153 <400> SEQUENCE: 2
154 Met Ala Ser Pro Ser Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp
155 1 5 10 15
157 His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
158 20 25 30
160 Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Gly Asn
161 35 40 45
163 Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
164 50 55 60
166 Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
167 65 70 75 80
169 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
170 85 90 95
172 Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr
173 100 105 110
175 Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
176 115 120 125
178 Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
179 130 135 140
181 Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
182 145 150 155 160
184 Val Thr Ser Ala Leu Val Ala Leu Pro Leu Phe Ala Met Gly Thr
185 165 170 175
187 Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn
188 180 185 190
190 Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser
191 195 200 205
193 Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile
194 210 215 220
196 Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe
197 225 230 235 240
199 Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser
200 245 250 255
202 Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu
203 260 265 270

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VERIFICATION SUMMARY

DATE: 08/18/2000

PATENT APPLICATION: US/09/635,521

TIME: 14:12:08

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\08182000\I635521.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:404 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:404 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3